

RAW SEQUENCE LISTING

EFS

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Application Serial Number: 10/561,906

Source: JWD

Date Processed by STIC: 3/28/07

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/561,906

DATE: 03/28/2007

TIME: 14:52:59.

Input Set : N:\efs\03_28_07\10561906_efs\281642US0XPCTST25.txt
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3 <110> APPLICANT: Patek, Miroslav
 4 Elisakova, Veronika
 6 <120> TITLE OF INVENTION: FEEDBACK RESISTANT ACETOHYDROXY ACID SYNTHETHASE MUTANTS
 8 <130> FILE REFERENCE: 281642US0XPCT
 10 <140> CURRENT APPLICATION NUMBER: US 10/561,906
 11 <141> CURRENT FILING DATE: 2005-12-21
 13 <150> PRIOR APPLICATION NUMBER: PCT/EP04/06157
 14 <151> PRIOR FILING DATE: 2004-06-08
 16 <150> PRIOR APPLICATION NUMBER: EP 03014640.1
 17 <151> PRIOR FILING DATE: 2003-06-26
 19 <160> NUMBER OF SEQ ID NOS: 12
 21 <170> SOFTWARE: PatentIn version 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 519
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Synthetic DNA
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
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 39 1 5 10 15
 41 gac gta gac gat gac ttt tcc cgc gta tca ggt atg ttc acc cga cgc 96
 42 Asp Val Asp Asp Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg
 43 20 25 30
 45 gca ttc aac ctc gtg tcc ctc gtg tct gca aag acc gaa aca cac ggc 144
 46 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
 47 35 40 45
 49 atc aac cgc atc acg gtt gtc gac gcc gac gag ctc aac att gag 192
 50 Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
 51 50 55 60
 53 cag atc aac aag cag ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg 240
 54 Gln Ile Asn Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
 55 65 70 75 80
 57 cga ctt gat gaa gag acc act atc gcc cgc gca atc atg ctg gtt aag 288
 58 Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
 59 85 90 95
 61 gtc tct gcg gac agc acc aac cgt ccg cag atc gtc gac gcc gcg aac 336
 62 Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
 63 100 105 110

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65 atc ttc cgc gcc cga gtc gtc gac gtg gct cca gac tct gtg gtt att	384
66 Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile	
67 115 120 125	
69 gaa tcc aca ggc acc cca ggc aag ctc cgc gca ctg ctt gac gtg atg	432
70 Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met	
71 130 135 140	
73 gaa caa ttc gaa atc cgc gaa ctg atc caa tcc gga cag att gca ctc	480
74 Glu Gln Phe Glu Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu	
75 145 150 155 160	
77 aac cgc ggt ccg aag acc atg gct ccg gcc aag atc taa	519
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96 Asp Val Asp Asp Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg	
97 20 25 30	
100 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly	
101 35 40 45	
104 Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu	
105 50 55 60	
108 Gln Ile Asn Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val	
109 65 70 75 80	
112 Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys	
113 85 90 95	
116 Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn	
117 100 105 110	
120 Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile	
121 115 120 125	
124 Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met	
125 130 135 140	
128 Glu Gln Phe Glu Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu	
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145 <220> FEATURE:	
146 <221> NAME/KEY: CDS	

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 152 1 5 10 15
 154 gac gta gac ggt gac ttt tcc cgc gta tca ggt atg ttc acc cga cgc 96
 155 Asp Val Asp Gly Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg
 156 20 25 30
 158 gca ttc aac ctc gtg tcc ctc gtg tct gca aag acc gaa aca cac ggc 144
 159 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
 160 35 40 45
 162 atc aac cgc atc acg gtt gtt gtc gac gcc gag ctc aac att gag 192
 163 Ile Asn Arg Ile Thr Val Val Asp Ala Asp Glu Leu Asn Ile Glu
 164 50 55 60
 166 cag atc acc aag cag ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg 240
 167 Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
 168 65 70 75 80
 170 cga ctt gat gaa gag acc act atc gcc cgc gca atc atg ctg gtt aag 288
 171 Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
 172 85 90 95
 174 gtc tct gcg gac agc acc aac cgt ccg cag atc gtc gac gcc gcg aac 336
 175 Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
 176 100 105 110
 178 atc ttc cgc gcc cga gtc gac gtg gct cca gac tct gtg gtt att 384
 179 Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
 180 115 120 125
 182 gaa tcc aca ggc acc cca ggc aag ctc cgc gca ctg ctt gac gtg atg 432
 183 Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
 184 130 135 140
 186 gaa cca tcc gga atc gcg gaa ctg atc caa tcc gga cag att gca ctc 480
 187 Glu Pro Ser Gly Ile Ala Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
 188 145 150 155 160
 190 aac cgc ggt ccg aag acc atg gct ccg gcc aag atc taa 519
 191 Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
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 196 <211> LENGTH: 172
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 - 201 <223> OTHER INFORMATION: Synthetic Construct
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 209 Asp Val Asp Gly Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg
 210 20 25 30
 213 Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
 214 35 40 45
 217 Ile Asn Arg Ile Thr Val Val Asp Ala Asp Glu Leu Asn Ile Glu

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218	50	55	60	
221	Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val			
222	65	70	75	80
225	Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys			
226	85	90	95	
229	Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn			
230	100	105	110	
233	Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile			
234	115	120	125	
237	Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met			
238	130	135	140	
241	Glu Pro Ser Gly Ile Ala Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu			
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245	Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile			
246	165	170		
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250	<211> LENGTH: 17			
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275	<212> TYPE: DNA			
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Input Set : N:\efs\03_28_07\10561906_efs\281642US0XPCTST25.txt
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320 Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg
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325 35 40 45
328 Ile Asn Arg Ile Thr Val Val Val Asp
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337 <400> SEQUENCE: 11
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356 <211> LENGTH: 57
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358 <213> ORGANISM: Escherichia Coli
360 <400> SEQUENCE: 12
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366 Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg
367 20 25 30
370 Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp
371 35 40 45
374 Lys Ser His Ile Trp Leu Leu Val Asn
375 50 55

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VERIFICATION SUMMARY
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